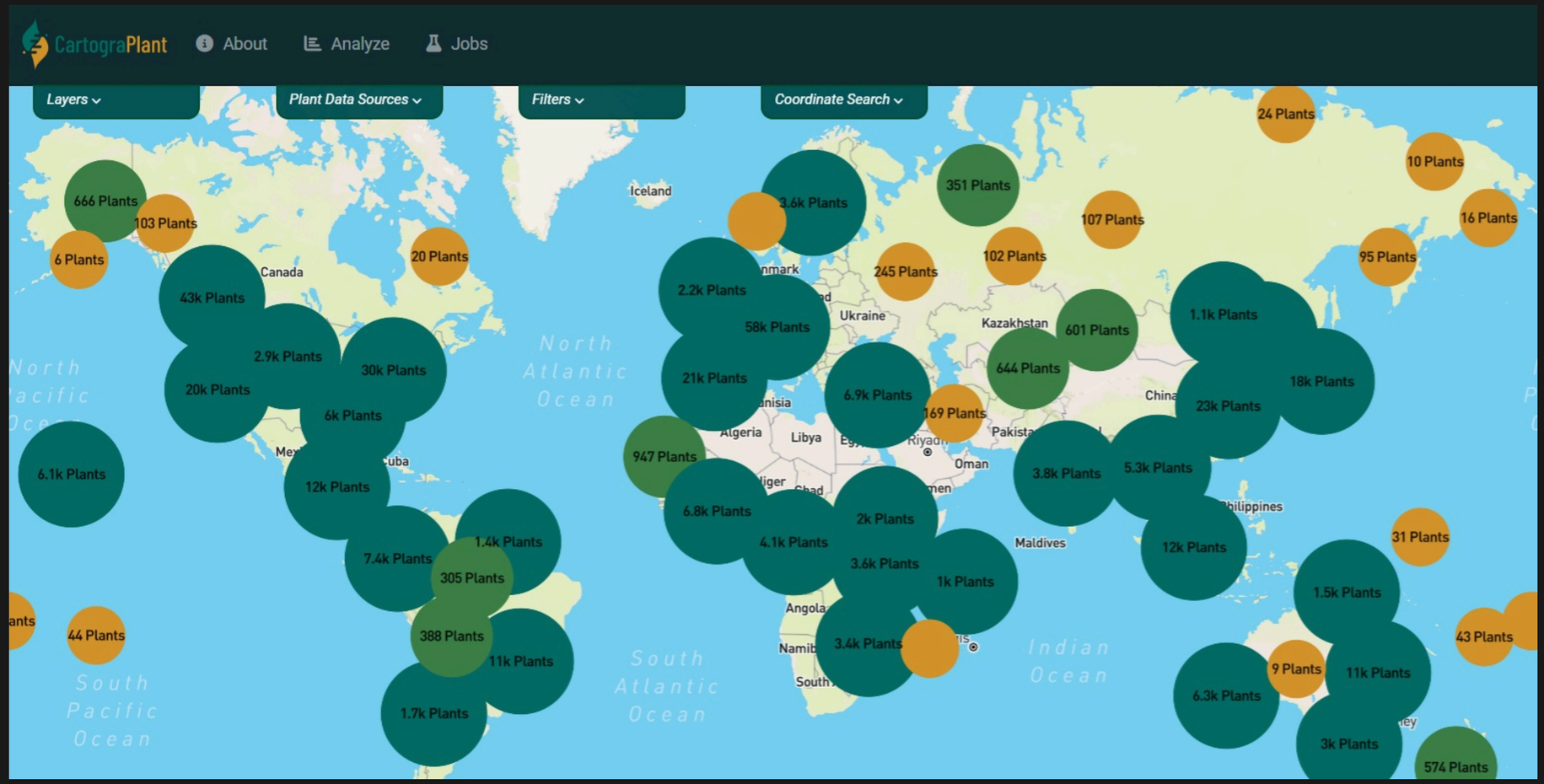
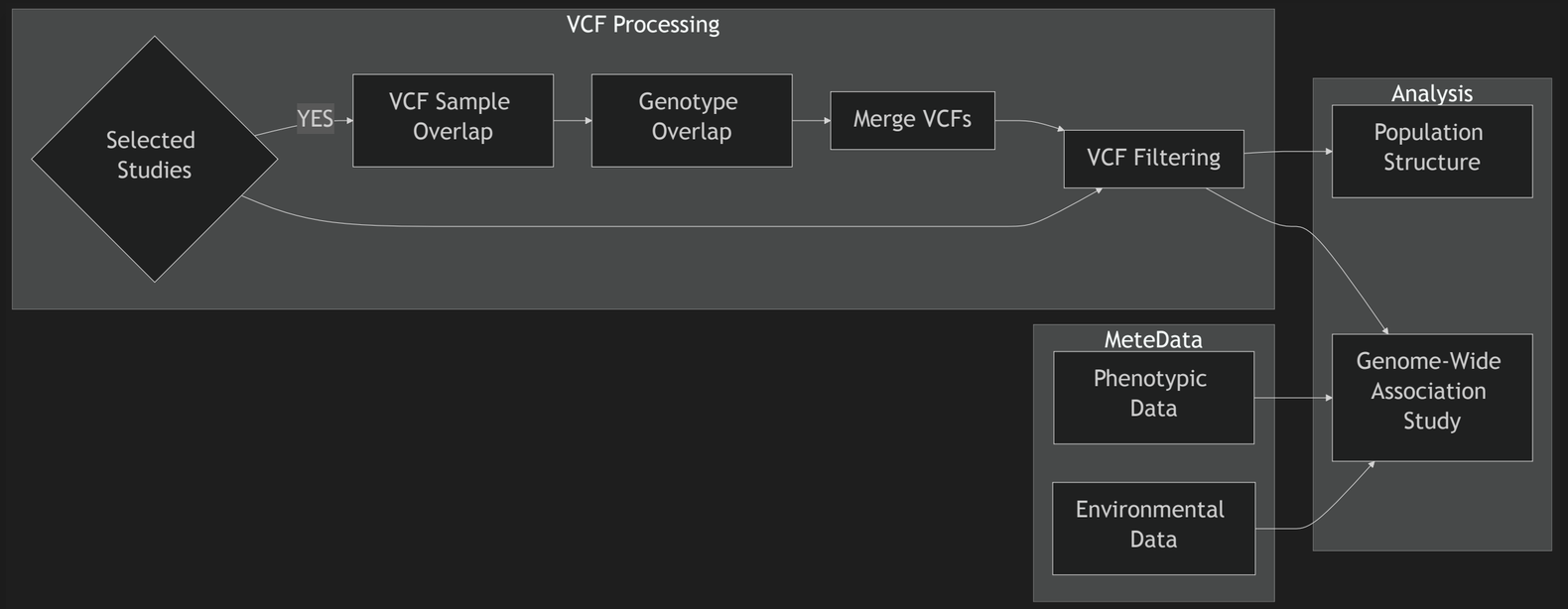
| Analysis Panel | Landscape Genomics | Demo |

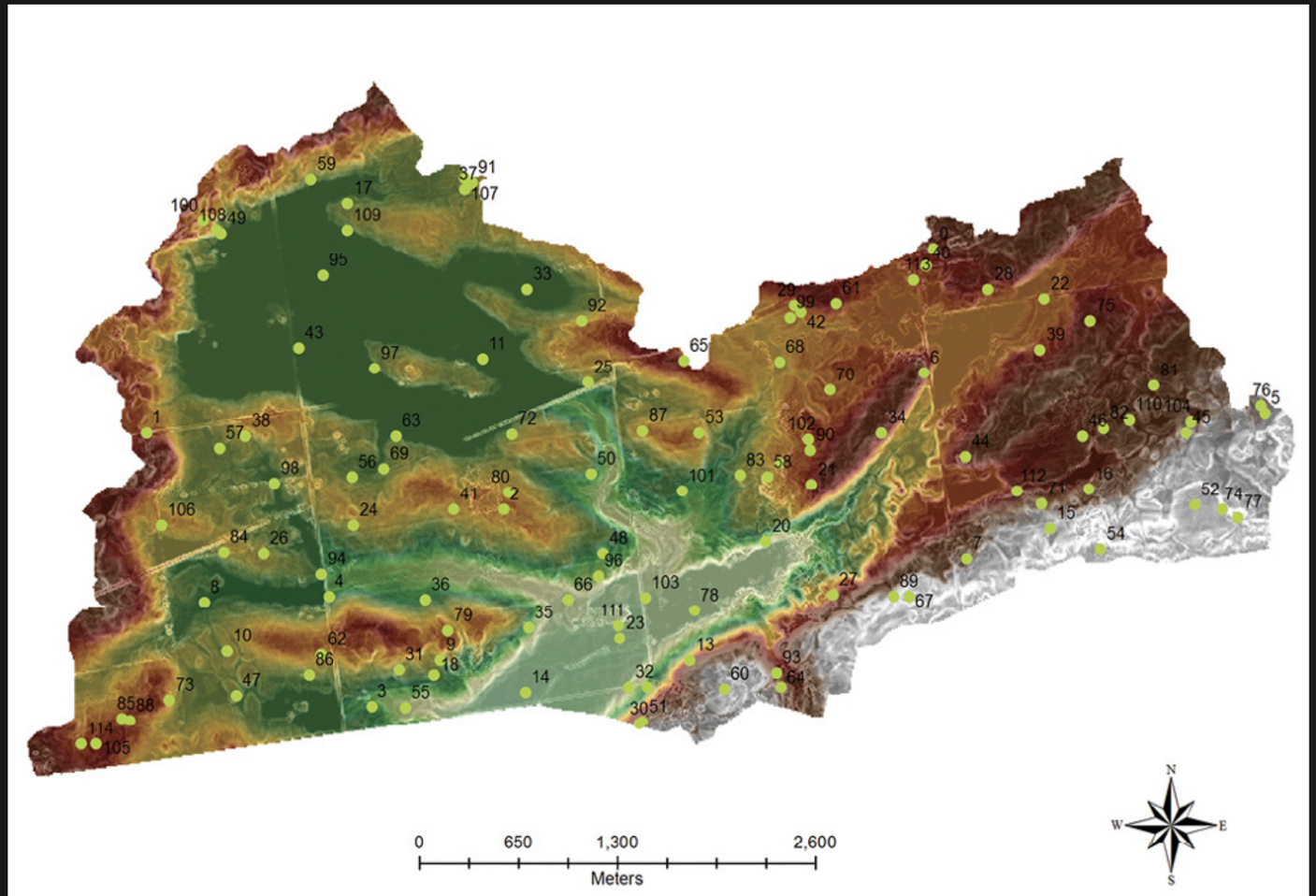


ANALYSIS PANEL OVERVIEW



LANDSCAPE GENOMICS

Aims to understand how environmental heterogeneity influences the distribution of genetic diversity.



POPULATION STRUCTURE

Patterns of genetic variation within and between individuals

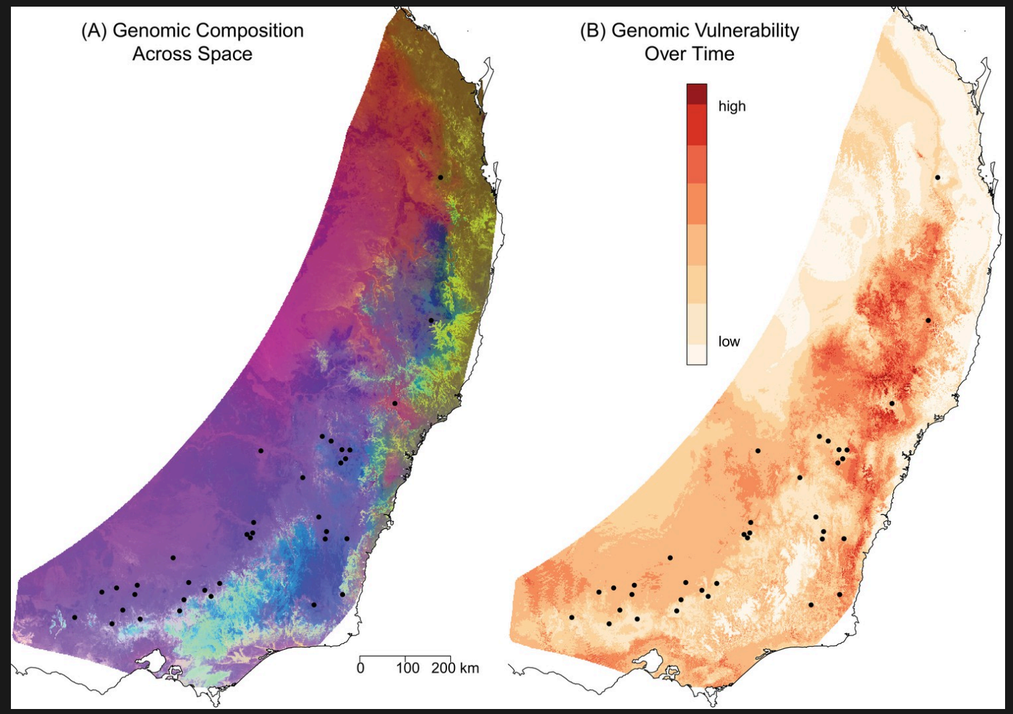
- Isolation by distance
- Genetic drift
- Selection

GENOME-WIDE ASSOCIATION STUDY (GWAS)

examines the relationship between different genotypes and specfic traits or environments

GENETIC OFFSET

Difference between the current genetic makeup to the genetic makeup predicted to be optimal for future environmental conditions



TPPS SUBMISSION ENABLES SEAMLESS INTEGRATION OF STUDIES

Allowing for analysis of large datasets in the analysis panel

Mega:
Integration of raw data

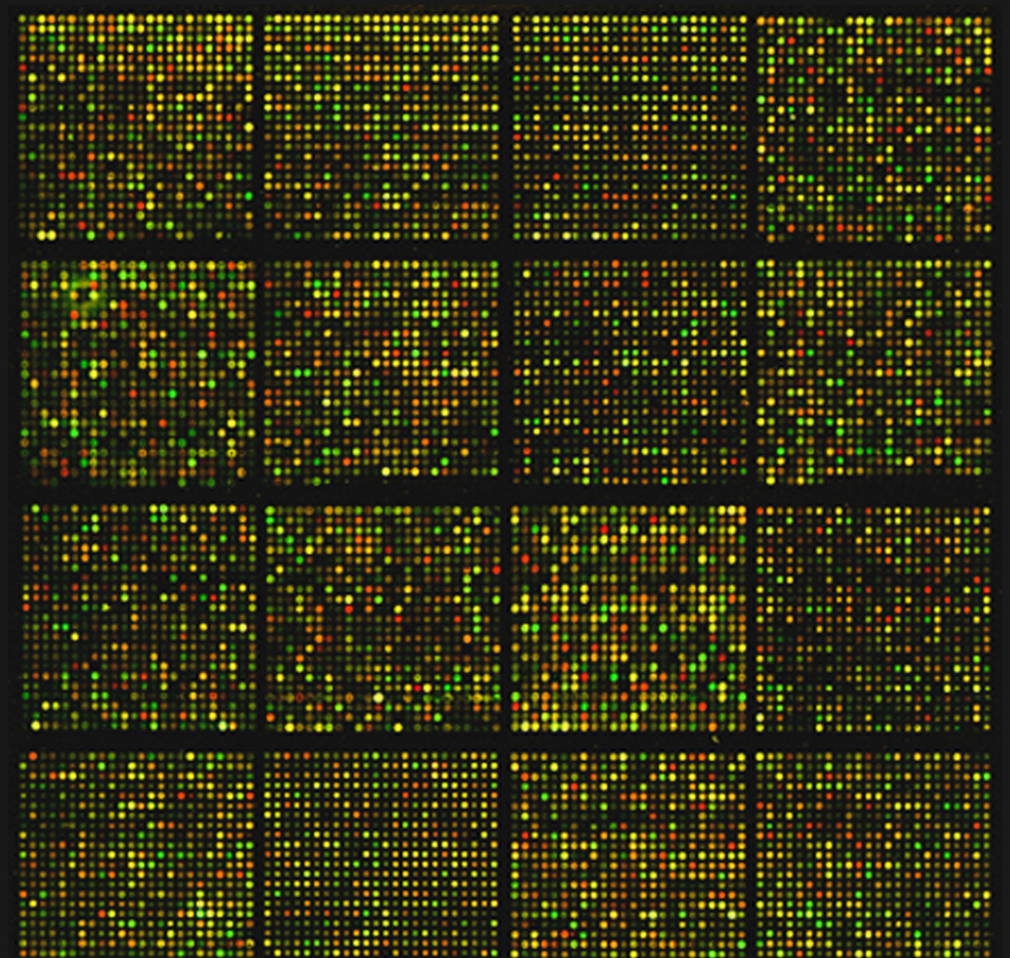
Meta:
Integration of summary results

DEMO WITH POPULUS TRICHOCARPA

Study	Samples	Genotypes	Phenotypes
Geraldes et al. 2008	55	32,000	0
Mckown et al. 2013	555	0	400
Mckown et al. 2014	555	28,000	0

DNA MICROARRAY

A cost effective way to obtain tens of thousands of mutations



NEXTFLOW

Workflow management software

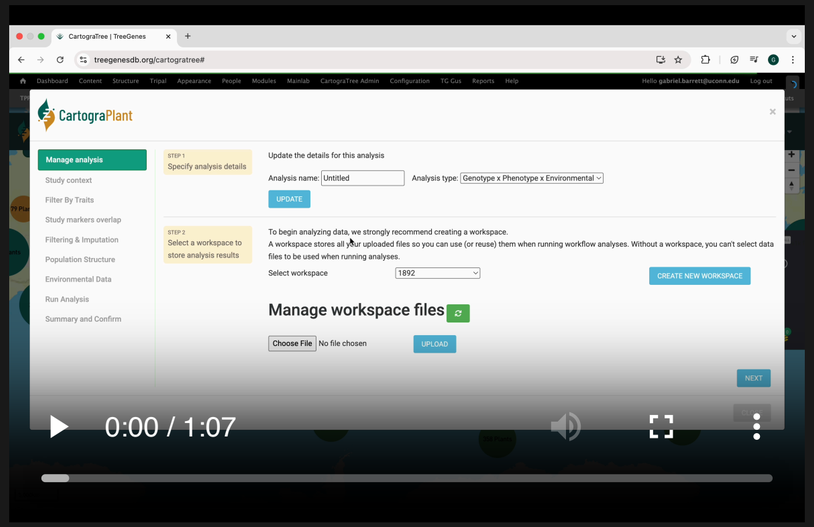
- Reproducible
- Concurrency
- Portable
- nf-core Community

Containerized Workflows Enable Reproducibility 🔁

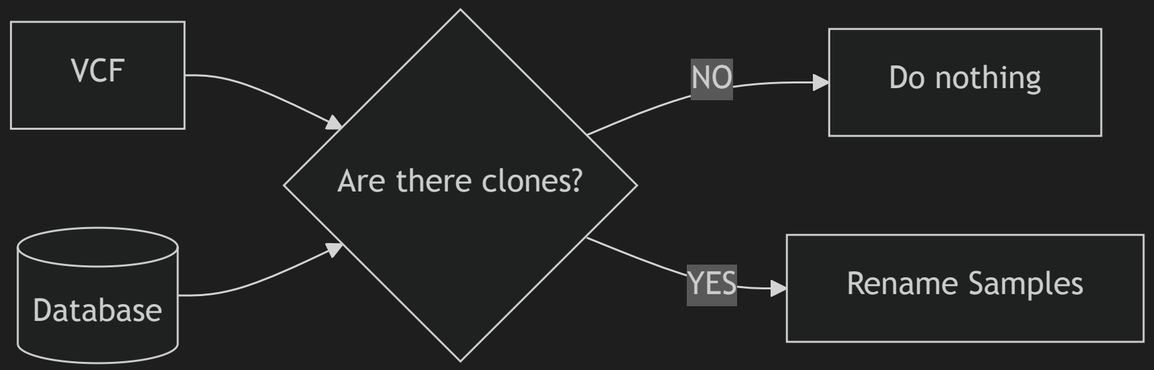
```
process FASTSTRUCTURE_VIS {
  label "process_low"

  container "${ workflow.containerEngine == 'singularity' &
    'https://depot.galaxyproject.org/singularity/mulled-v2-
    'biocontainers/mulled-v2-c85b516872f711516305474353432f

  input:
  path meanQ
  path samples

  output:
  path "*.png", emit: png

  when:
```

WORKSPACE

File management


CartograTree | TreeGenes
treegenesdb.org/cartogratree#
Dashboard Content Structure Tripal Appearance People Modules Mainlab CartograTree Admin Configuration TC Gus Reports Help
Hello gabriel.barrett@uconn.edu Log out
CartograPlant
Manage analysis
Study context
Filter By Traits
Study markers overlap
Filtering & Imputation
Population Structure
Environmental Data
Run Analysis
Summary and Confirm
STEP 1
Specify analysis details
Update the details for this analysis
Analysis name: Untitled
Analysis type: Genotype x Phenotype x Environmental
UPDATE
STEP 2
Select a workspace to store analysis results
To begin analyzing data, we strongly recommend creating a workspace.
A workspace stores all your uploaded files so you can use (or reuse) them when running workflow analyses. Without a workspace, you can't select data files to be used when running analyses.
Select workspace
1892
CREATE NEW WORKSPACE
Manage workspace files
Choose File
No file chosen
UPLOAD
NEXT
0:00 / 1:07

STUDY-CONTEXT



Study 1	Study 2	Study 3	Standard Name
GLCA-26-1	GLCA26-1	GLCA26-1	sample05
HFCA-20-2	Null	Null	sample06

Video

FILTER BY TRAITS

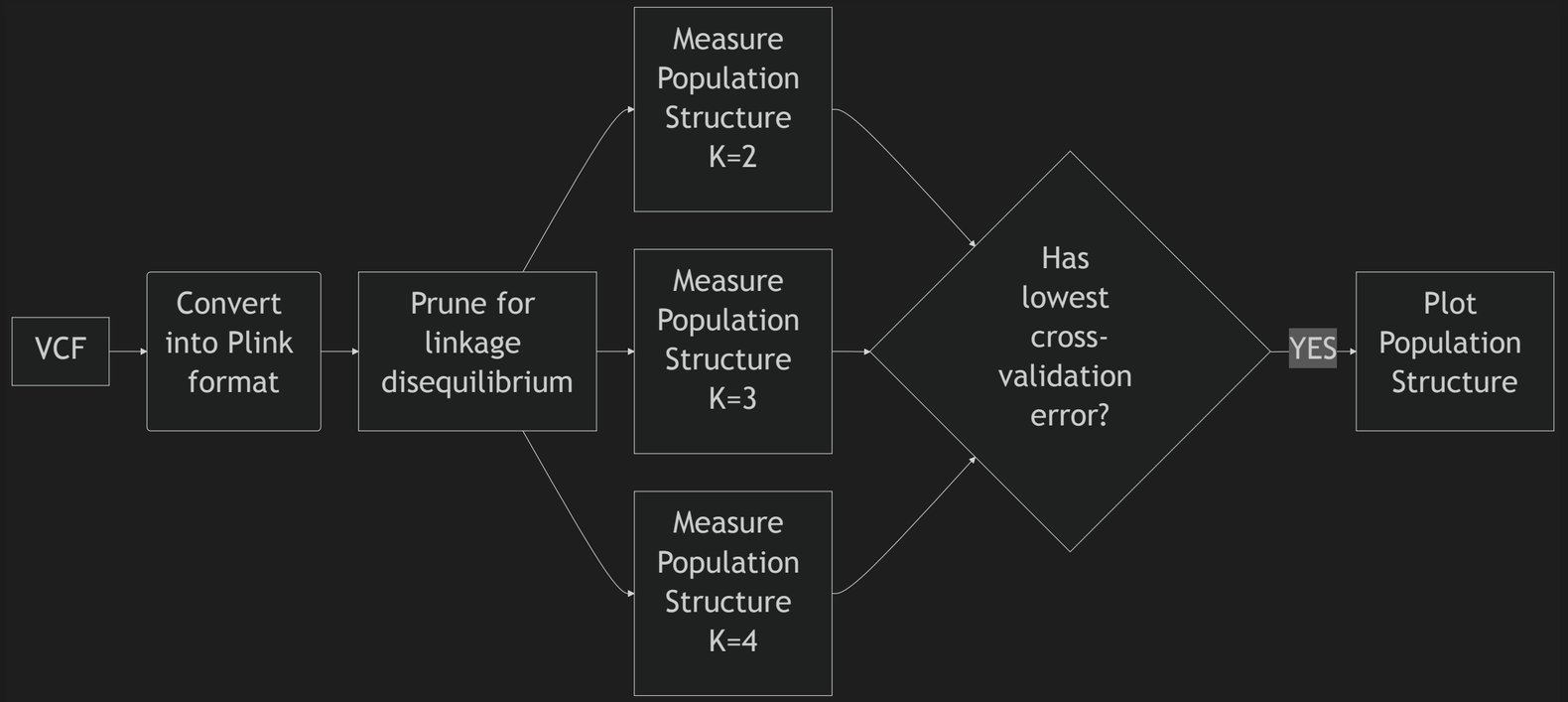
Select phenotypes of interest for upload into workspace

- Determine total counts
- Redundancy analysis based on x>1 phenotypes

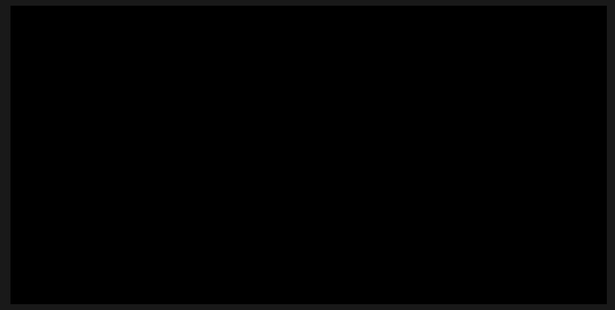
STUDY MARKERS OVERLAP

1. Genotype concordance
2. Merge VCF's

POPULATION STRUCTURE



DEMO



CHOOSE ENVIRONMENTS

RUN ANALYSIS

Perform G x P and G x E associations

TIMELINE